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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/485,473

DATE: 09/10/2001
TIME: 11:00:27

Input Set : A:\10496p61.app
Output Set: N:\CRF3\09102001\I485473.raw

ENTERED

p. 5

```
 3 <110> APPLICANT: STOFFEL, WILHELM
 4        HOFMANN, KAY
 5        TOMIUK, STEPHAN
 7 <120> TITLE OF INVENTION: NEUTRAL SPHINGOMYELINASE
 9 <130> FILE REFERENCE: 10496/P61950US1
11 <140> CURRENT APPLICATION NUMBER: 09/485,473
12 <141> CURRENT FILING DATE: 2000-02-11
14 <160> NUMBER OF SEQ ID NOS: 6
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 423
20 <212> TYPE: PRT
21 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
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25  1               5                  10                  15
27 Trp Gly Ile Pro Tyr Leu Ser Lys His Arg Ala Asp Arg Met Arg Arg
28              20                  25                  30
30 Leu Gly Asp Phe Leu Asn Gln Glu Ser Phe Asp Leu Ala Leu Leu Glu
31          35                  40                  45
33 Glu Val Trp Ser Glu Gln Asp Phe Gln Tyr Leu Arg Gln Lys Leu Ser
34      50                  55                  60
36 Pro Thr Tyr Pro Ala Ala His His Phe Arg Ser Gly Ile Ile Gly Ser
37  65                  70                  75                  80
39 Gly Leu Cys Val Phe Ser Lys His Pro Ile Gln Glu Leu Thr Gln His
40              85                  90                  95
42 Ile Tyr Thr Leu Asn Gly Tyr Pro Tyr Met Ile His His Gly Asp Trp
43          100                 105                 110
45 Phe Ser Gly Lys Ala Val Gly Leu Leu Val Leu His Leu Ser Gly Met
46          115                 120                 125
48 Val Leu Asn Ala Tyr Val Thr His Leu His Ala Glu Tyr Asn Arg Gln
49      130                 135                 140
51 Lys Asp Ile Tyr Leu Ala His Arg Val Ala Gln Ala Trp Glu Leu Ala
52 145                 150                 155                 160
54 Gln Phe Ile His His Thr Ser Lys Lys Ala Asp Val Val Leu Leu Cys
55              165                 170                 175
57 Gly Asp Leu Asn Met His Pro Glu Asp Leu Gly Cys Cys Leu Leu Lys
58              180                 185                 190
60 Glu Trp Thr Gly Leu His Asp Ala Tyr Leu Glu Thr Arg Asp Phe Lys
61          195                 200                 205
63 Gly Ser Glu Glu Gly Asn Thr Met Val Pro Lys Asn Cys Tyr Val Ser
64      210                 215                 220
66 Gln Gln Glu Leu Lys Pro Phe Pro Phe Gly Val Arg Ile Asp Tyr Val
67 225                 230                 235                 240
69 Leu Tyr Lys Ala Val Ser Gly Phe Tyr Ile Ser Cys Lys Ser Phe Glu
70              245                 250                 255
72 Thr Thr Thr Gly Phe Asp Pro His Ser Gly Thr Pro Leu Ser Asp His
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73              260                265                270
75 Glu Ala Leu Met Ala Thr Leu Phe Val Arg His Ser Pro Pro Gln Gln
76          275                280                285
78 Asn Pro Ser Ser Thr His Gly Pro Ala Glu Arg Ser Pro Leu Met Cys
79      290                295                300
81 Val Leu Lys Glu Ala Trp Thr Glu Leu Gly Leu Gly Met Ala Gln Ala
82 305              310                315                320
84 Arg Trp Trp Ala Thr Phe Ala Ser Tyr Val Ile Gly Leu Gly Leu Leu
85              325                330                335
87 Leu Leu Ala Leu Leu Cys Val Leu Ala Ala Gly Gly Gly Ala Gly Glu
88          340                345                350
90 Ala Ala Ile Leu Leu Trp Thr Pro Ser Val Gly Leu Val Leu Trp Ala
91      355                360                365
93 Gly Ala Phe Tyr Leu Phe His Val Gln Glu Val Asn Gly Leu Tyr Arg
94      370                375                380
96 Ala Gln Ala Glu Leu Gln His Val Leu Gly Arg Ala Arg Glu Ala Gln
97 385              390                395                400
99 Asp Leu Gly Pro Glu Pro Gln Pro Ala Leu Leu Leu Gly Gln Gln Glu
100             405                410                415
102 Gly Asp Arg Thr Lys Glu Gln
103             420
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 419
108 <212> TYPE: PRT
109 <213> ORGANISM: Murine sp.
111 <400> SEQUENCE: 2
112 Met Lys Leu Asn Phe Ser Leu Arg Leu Arg Val Phe Asn Leu Asn Cys
113  1              5                10                15
115 Trp Asp Ile Pro Tyr Leu Ser Lys His Arg Ala Asp Arg Met Lys Arg
116             20                25                30
118 Leu Gly Asp Phe Leu Asn Leu Glu Asn Phe Asp Leu Ala Leu Leu Glu
119          35                40                45
121 Glu Val Trp Ser Glu Gln Asp Phe Gln Tyr Leu Arg Gln Arg Leu Ser
122      50                55                60
124 Leu Thr Tyr Pro Asp Ala His Tyr Phe Arg Ser Gly Met Ile Gly Ser
125 65              70                75                80
127 Gly Leu Cys Val Phe Ser Lys His Pro Ile Gln Glu Ile Phe Gln His
128             85                90                95
130 Val Tyr Ser Leu Asn Gly Tyr Pro Tyr Met Phe His His Gly Asp Trp
131             100                105                110
133 Phe Cys Gly Lys Ser Val Gly Leu Leu Val Leu Arg Leu Ser Gly Leu
134          115                120                125
136 Val Leu Asn Ala Tyr Val Thr His Leu His Ala Glu Tyr Ser Arg Gln
137      130                135                140
139 Lys Asp Ile Tyr Phe Ala His Arg Val Ala Gln Ala Trp Glu Leu Ala
140 145              150                155                160
142 Gln Phe Ile His His Thr Ser Lys Asn Ala Asp Val Val Leu Leu Cys
143              165                170                175
145 Gly Asp Leu Asn Met His Pro Lys Asp Leu Gly Cys Cys Leu Leu Lys
```

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```
146           180              185              190
148 Glu Trp Thr Gly Leu His Asp Ala Phe Val Glu Thr Glu Asp Phe Lys
149           195              200              205
151 Gly Ser Asp Asp Gly Cys Thr Met Val Pro Lys Asn Cys Tyr Val Ser
152      210              215              220
154 Gln Gln Asp Leu Gly Pro Phe Pro Ser Gly Ile Arg Ile Asp Tyr Val
155 225              230              235              240
157 Leu Tyr Lys Ala Val Ser Glu Phe His Val Cys Cys Glu Thr Leu Lys
158           245              250              255
160 Thr Thr Thr Gly Cys Asp Pro His Ser Asp Lys Pro Phe Ser Asp His
161           260              265         ·    270
163 Glu Ala Leu Met Ala Thr Leu Tyr Val Lys His Ser Pro Pro Gln Glu
164      275              280              285
166 Asp Pro Cys Thr Ala Cys Gly Pro Leu Glu Arg Ser Asp Leu Ile Ser
167      290              295              300
169 Val Leu Arg Glu Ala Arg Thr Glu Leu Gly Leu Gly Ile Ala Lys Ala
170 305              310              315    .         320
172 Arg Trp Trp Ala Ala Phe Ser Gly Tyr Val Ile Val Trp Gly Leu Ser
173           325              330              335
175 Leu Leu Val Leu Leu Cys Val Leu Ala Ala Gly Glu Glu Ala Arg Glu
176           340              345              350
178 Val Ala Ile Ile Leu Cys Ile Pro Ser Val Gly Leu Val Leu Val Ala
179      355              360              365
181 Gly Ala Val Tyr Leu Phe His Lys Gln Glu Ala Lys Gly Leu Cys Arg
182      370              375              380
184 Ala Gln Ala Glu Met Leu His Val Leu Thr Arg Glu Thr Glu Thr Gln
185 385              390              395              400
187 Asp Arg Gly Ser Glu Pro His Leu Ala Tyr Cys Leu Gln Gln Glu Gly
188           405              410              415
190 Asp Arg Ala
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194 <211> LENGTH: 1662
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 3
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200 ggcgctctcc ggaccccccag ggtcctagcg cgcggcccctt accgagcctg ggcgcccgga 120
201 tttcggsagc ggatcgcctt tccgggttgg cggcccgcct gattgggaac agccggccgg 180
202 ttgccggggg aacgcgggag tcgggcccga cctgagccac gcgggcttgg tgcccacctg 240
203 tgcgcgccgc ctgcgaagaa ggaacggtct agggagaagg cgccgccggc cgccccccgtc 300
204 cccaccgcgg ccgtcgctgg agagttcgag ccgcctagcg cccctggagc tccccaacca 360
205 tgaagctcaa cttctccctg cgactgcgga tcttcaacct caactgctgg ggcattccgt 420
206 acttgagcaa gcaccgggcc gaccgcatga ggcgcctggg agactttctg aaccaggaga 480
207 gcttcgacct ggctttgctg gaggaggtgt ggagtgagca ggacttccag tacctgagac 540
208 agaagctgtc acctacctac ccagctgcac accacttccg gagcggaatc attggcagtg 600
209 gcctctgtgt cttctccaaa catccaatcc aggagcttac ccagcacatc tacactctca 660
210 atggctaccc ctacatgatc catcatggtg actggttcag tgggaaggct gtggggctgc 720
211 tggtgctcca tctaagtggc atggtgctca acgcctatgt gacccatctc catgccgaat 780
212 acaatcgaca gaaggacatc tacctagcac atcgtgtggc ccaagcttgg gaattggccc 840
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213 agttcatcca ccacacatcc aagaaggcag acgtggttct gttgtgtgga gacctcaaca 900
214 tgcacccaga agacctgggc tgctgcctgc tgaaggagtg gacagggctt catgatgcct 960
215 atcttgaaac tcgggacttc aagggctctg aggaaggcaa cacaatggta cccaagaact 1020
216 gctacgtcag ccagcaggag ctgaagccat ttccctttgg tgtccgcatt gactacgtgc 1080
217 tttacaaggc agtttctggg ttttacatct cctgtaagag ttttgaaacc actacaggct 1140
218 ttgaccctca cagtggcacc cccctctctg atcatgaagc cctgatggct actctgtttg 1200
219 tgaggcacag ccccccacag cagaaccccca gctctaccca cggaccagca gagaggtcgc 1260
220 cgttgatgtg tgtgctaaag gaggcctgga cggagctggg tctgggcatg gctcaggctc 1320
221 gctggtgggc caccttcgct agctatgtga ttggcctggg gctgcttctc ctggcactgc 1380
222 tgtgtgtcct ggcggctgga ggaggggccg gggaagctgc catactgctc tggacccctca 1440
223 gtgtagggct ggtgctgtgg gcaggtgcat tctacctctt ccacgtacag gaggtcaatg 1500
224 gcttatatag ggcccaggct gagctccagc atgtgctagg aagggcaagg gaggcccagg 1560
225 atctgggccc agagcctcag ccagccctac tcctggggca gcaggagggg gacagaacta 1620
226 aagaacaata aagcttggcc ctttaaaaaa aaaaaaaaaa aa                      1662
229 <210> SEQ ID NO: 4
230 <211> LENGTH: 1627
231 <212> TYPE: DNA
232 <213> ORGANISM: Murine sp.
234 <400> SEQUENCE: 4
235 gtgctggtgg aagccgagcc gggaacaagg gaggaacctg taggccgcgg tgcgagaacc 60
236 caccgaagac ctaagaatct ggaacagtcc acccgagatt ccttccagga ctgccggcgg 120
237 ctcgcgcacc agcccgggat ttgcagccga ccttctttcc gggtggaagg acggcctttg 180
238 tcccagtaac gcaggagtcg cccccccaccc ccaaccagct cgcgttcctg ggtcggggca 240
239 gcgcaggaca gggcaataag cctgtgcgcg caatccgcct cgccgcccctt gctccgaagc 300
240 actccagcca tgaagctcaa cttttctcta cggctgagag ttttcaatct caactgctgg 360
241 gacatcccct acctgagcaa acatagggcg gaccgcatga agcgcttggg agactttctg 420
242 aacttggaaa actttgatct ggctctcctg gaggaggtgt ggagtgagca ggacttccag 480
243 tacctaaggc aaaggctatc gctcacctat ccagatgcac actacttcag aagcgggatg 540
244 ataggcagtg gcctctgtgt gttctccaaa cacccaatcc aggaaatctt ccagcatgtc 600
245 tacagtctga atggttaccc ctacatgttc catcatggag actggttctg tgggaagtct 660
246 gtggggctgc tggtgctccg tctaagtgga ctggtgctca atgcctacgt gactcatcta 720
247 catgctgagt acagccgaca gaaggacatc tactttgcac accgtgtggc ccaagcttgg 780
248 gaactggccc agttcatcca ccacacatcc aagaatgcag atgtggttct attgtgtgga 840
249 gacctcaata tgcaccccaa agacctgggc tgctgcctgc tgaaagagtg gacagggctc 900
250 catgatgctt tcgttgagac tgaggacttt aagggctctg atgatggctg taccatggta 960
251 cccaagaact gctacgtcag ccagcaggac ctgggaccgt ttccgtctgg tatccggatt 1020
252 gattacgtgc tttacaaggc agtctctgag ttccacgtct gctgtgagac tctgaaaacc 1080
253 actacaggct gtgaccctca cagtgacaag cccttctctg atcacgaggc cctcatggct 1140
254 actttgtatg tgaagcacag ccccccctcag gaagacccct gtactgcctg tggcccactg 1200
255 gaaaggtccg atttgatcag cgtgctaagg gaggccagga cagagctggg gctaggcata 1260
256 gctaaagctc gctggtgggc tgcattctct ggctatgtga tcgtttgggg gctgtccctt 1320
257 ctggtgttgc tgtgtgtcct ggctgcagga gaagaggcca gggaagtggc catcatcctc 1380
258 tgcataccca gtgtgggtct ggtgctggta gcaggtgcag tctacctctt ccacaagcag 1440
259 gaggccaagg gcttatgtcg ggcccaggct gagatgctgc acgttctgac aagggaaacg 1500
260 gagacccagg accgaggctc agagcctcac ctagcctact gcttgcagca ggagggggac 1560
261 agagcttaag agcttaacaa taaaacttgc ttgacacaca aaaaaaaaaa aaaaaaaaaa 1620
262 aaaaaaa                                                            1627
265 <210> SEQ ID NO: 5
266 <211> LENGTH: 4464
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RAW SEQUENCE LISTING   DATE: 09/10/2001
PATENT APPLICATION: US/09/485,473   TIME: 11:00:27

Input Set : A:\10496p61.app
Output Set: N:\CRF3\09102001\I485473.raw

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267 <212> TYPE: DNA
268 <213> ORGANISM: Homo sapiens
270 <220> FEATURE:
271 <221> NAME/KEY: modified_base
272 <222> LOCATION: (2435)
273 <223> OTHER INFORMATION: a, t, c, g, other or unknown
275 <220> FEATURE:
276 <221> NAME/KEY: modified_base
277 <222> LOCATION: (2437)
278 <223> OTHER INFORMATION: a, t, c, g, other or unknown
280 <220> FEATURE:
281 <221> NAME/KEY: modified_base
282 <222> LOCATION: (2440)
283 <223> OTHER INFORMATION: a, t, c, g, other or unknown
285 <220> FEATURE:
286 <221> NAME/KEY: modified_base
287 <222> LOCATION: (3970)
288 <223> OTHER INFORMATION: a, t, c, g, other or unknown
290 <220> FEATURE:
291 <221> NAME/KEY: modified_base
292 <222> LOCATION: (4036)
293 <223> OTHER INFORMATION: a, t, c, g, other or unknown
295 <220> FEATURE:
296 <221> NAME/KEY: modified_base
297 <222> LOCATION: (4039)
298 <223> OTHER INFORMATION: a, t, c, g, other or unknown
300 <220> FEATURE:
301 <221> NAME/KEY: modified_base
302 <222> LOCATION: (4045)
303 <223> OTHER INFORMATION: a, t, c, g, other or unknown
305 <220> FEATURE:
306 <221> NAME/KEY: modified_base
307 <222> LOCATION: (4076)
308 <223> OTHER INFORMATION: a, t, c, g, other or unknown
310 <220> FEATURE:
311 <221> NAME/KEY: modified_base
312 <222> LOCATION: (4084)
313 <223> OTHER INFORMATION: a, t, c, g, other or unknown
315 <220> FEATURE:
316 <221> NAME/KEY: modified_base
317 <222> LOCATION: (4094)
318 <223> OTHER INFORMATION: a, t, c, g, other or unknown
320 <220> FEATURE:
321 <221> NAME/KEY: modified_base
322 <222> LOCATION: (4102)
323 <223> OTHER INFORMATION: a, t, c, g, other or unknown
325 <220> FEATURE:
326 <221> NAME/KEY: modified_base
327 <222> LOCATION: (4103)
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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY   DATE: 09/10/2001
PATENT APPLICATION: **US/09/485,473**   TIME: 11:00:28

Input Set : **A:\10496p61.app**
Output Set: **N:\CRF3\09102001\I485473.raw**

```
L:546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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